

SEQUENCE LISTING

<110> Galdes, Alphonse
Mahanthappa, Nagesh

<120> METHODS AND COMPOSITIONS FOR TREATING DISORDERS INVOLVING
EXCITOTOXICITY

<130> BIV-069.02

<140> 09/325,602

<141> 1999-06-03

<150> 09/238,243

<151> 1999-01-27

<160> 32

<170> PatentIn Ver. 2.1

<210> 1

<211> 1277

<212> DNA

<213> Gallus sp.

<220>

<221> CDS

<222> (1)..(1275)

<400> 1

atg gtc gaa atg ctg ctg ttg aca aga att ctc ttg gtg ggc ttc atc	48
Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile	
1 5 10 15	
tgc gct ctt tta gtc tcc tct ggg ctg act tgt gga cca ggc agg ggc	96
Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly	
20 25 30	
att gga aaa agg agg cac ccc aaa aag ctg acc ccg tta gcc tat aag	144
Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys	
35 40 45	
cag ttt att ccc aat gtg gca gag aag acc cta ggg gcc agt gga aga	192
Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg	
50 55 60	
tat gaa ggg aag atc aca aga aac tcc gag aga ttt aaa gaa cta acc	240
Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr	
65 70 75 80	
cca aat tac aac cct gac att att ttt aag gat gaa gag aac acg gga	288
Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly	
85 90 95	
gct gac aga ctg atg act cag cgc tgc aag gac aag ctg aat gcc ctg	336
Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu	
100 105 110	

gcg atc tcg gtg atg aac cag tgg ccc ggg gtg aag ctg cgg gtg acc	384
Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr	
115 120 125	
gag ggc tgg gac gag gat ggc cat cac tcc gag gaa tcg ctg cac tac	432
Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr	
130 135 140	
gag ggt cgc gcc gtg gac atc acc acg tgg gat cgg gac cgc agc aag	480
Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys	
145 150 155 160	
tac gga atg ctg gcc cgc ctc gcc gtc gag gcc ggc ttc gac tgg gtc	528
Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val	
165 170 175	
tac tac gag tcc aag gcg cac atc cac tgc tcc gtc aaa gca gaa aac	576
Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn	
180 185 190	
tca gtg gca gcg aaa tca gga ggc tgc ttc cct ggc tca gcc aga gtg	624
Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val	
195 200 205	
cac ctg gag cat gga ggc acc aag ctg gtg aag gac ctg agc cct ggg	672
His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly	
210 215 220	
gac cgc gtg ctg gct gct gac gcg gac ggc cgg ctg ctc tac agt gac	720
Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp	
225 230 235 240	
ttc ctc acc ttc ctc gac cgg atg gac agc tcc cga aag ctc ttc tac	768
Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr	
245 250 255	
gtc atc gag acg cgg cag ccc cgg gcc cgg ctg cta ctg acg gcg gcc	816
Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala	
260 265 270	
cac ctg ctc ttt gtg gcc ccc cag cac aac cag tcg gag gcc aca ggg	864
His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly	
275 280 285	
tcc acc agt ggc cag gcg ctc ttc gcc agc aac gtg aag cct ggc caa	912
Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln	
290 295 300	
cgt gtc tat gtg ctg ggc gag ggc ggg cag cag ctg ctg ccg gcg tct	960
Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser	
305 310 315 320	
gtc cac agc gtc tca ttg cgg gag gag gcg tcc gga gcc tac gcc cca	1008
Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro	
325 330 335	

ctc acc gcc cag ggc acc atc ctc atc aac cgg gtg ttg gcc tcc tgc	1056
Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys	
340 345 350	
tac gcc gtc atc gag gag cac agt tgg gcc cat tgg gcc ttc gca cca	1104
Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro	
355 360 365	
ttc cgc ttg gct cag ggg ctg ctg gcc gcc ctc tgc cca gat ggg gcc	1152
Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala	
370 375 380	
atc cct act gcc gcc acc acc acc act ggc atc cat tgg tac tca cgg	1200
Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg	
385 390 395 400	
ctc ctc tac cgc atc ggc agc tgg gtg ctg gat ggt gac gcg ctg cat	1248
Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His	
405 410 415	
ccg ctg ggc atg gtg gca ccg gcc agc tg	1277
Pro Leu Gly Met Val Ala Pro Ala Ser	
420 425	
<210> 2	
<211> 1190	
<212> DNA	
<213> Murine sp.	
<220>	
<221> CDS	
<222> (1)..(1188)	
<400> 2	
atg gct ctg ccg gcc agt ctg ttg ccc ctg tgc tgc ttg gca ctc ttg	48
Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu	
1 5 10 15	
gca cta tct gcc cag agc tgc ggg ccg ggc cga gga ccg gtt ggc cgg	96
Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg	
20 25 30	
cgg cgt tat gtg cgc aag caa ctt gtg cct ctg cta tac aag cag ttt	144
Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe	
35 40 45	
gtg ccc agt atg ccc gag cgg acc ctg ggc gcg agt ggg cca gcg gag	192
Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu	
50 55 60	
ggg agg gta aca agg ggg tcg gag cgc ttc cgg gac ctc gta ccc aac	240
Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn	
65 70 75 80	
tac aac ccc gac ata atc ttc aag gat gag gag aac agc ggc gca gac	288
Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp	
85 90 95	

cgc ctg atg aca gag cgt tgc aaa gag cgg gtg aac gct cta gcc atc	336
Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile	
100 105 110	
gcg gtg atg aac atg tgg ccc gga gta cgc cta cgt gtg act gaa ggc	384
Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly	
115 120 125	
tgg gac gag gac ggc cac cac gca cag gat tca ctc cac tac gaa ggc	432
Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly	
130 135 140	
cgt gcc ttg gac atc acc acg tct gac cgt gac cgt aat aag tat ggt	480
Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly	
145 150 155 160	
ttg ttg gcg cgc cta gct gtg gaa gcc gga ttc gac tgg gtc tac tac	528
Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr	
165 170 175	
gag tcc cgc aac cac atc cac gta tcg gtc aaa gct gat aac tea ctg	576
Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu	
180 185 190	
gcg gtc cga gcc gga ggc tgc ttt ccg gga aat gcc acg gtg cgc ttg	624
Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu	
195 200 205	
cgg agc ggc gaa cgg aag ggg ctg agg gaa cta cat cgt ggt gac tgg	672
Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp	
210 215 220	
gta ctg gcc gct gat gca gcg ggc cga gtg gta ccc acg cca gtg ctg	720
Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu	
225 230 235 240	
ctc ttc ctg gac cgg gat ctg cag cgc cgc gcc tcg ttc gtg gct gtg	768
Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val	
245 250 255	
gag acc gag cgg cct ccg cgc aaa ctg ttg ctc aca ccc tgg cat ctg	816
Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu	
260 265 270	
gtg ttc gct gct cgc ggg cca gcg cct gct cca ggt gac ttt gca ccg	864
Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro	
275 280 285	
gtg ttc gcg cgc cgc tta cgt gct ggc gac tcg gtg ctg gct ccc ggc	912
Val Phe Ala Arg Arg Leu Ala Gly Asp Ser Val Leu Ala Pro Gly	
290 295 300	
ggg gac gcg ctc cag ccg gcg cgc gta gcc cgc gtg gcg cgc gag gaa	960
Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu	
305 310 315 320	

gcc gtg ggc gtg ttc gca ccg ctc act gcg cac ggg acg ctg ctg gtc 1008
Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
325 330 335

aac gac gtc ctc gcc tcc tgc tac gcg gtt cta gag agt cac cag tgg 1056
Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
340 345 350

gcc cac cgc gcc ttc gcc cct ttg cgg ctg ctg cac gcg ctc ggg gct 1104
Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
355 360 365

ctg ctc cct ggg ggt gca gtc cag ccg act ggc atg cat tgg tac tct 1152
Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
370 375 380

cgc ctc ctt tac cgc ttg gcc gag gag tta atg ggc tg 1190
Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
385 390 395

<210> 3
<211> 1281
<212> DNA
<213> Murine sp.

<220>
<221> CDS
<222> (1)..(1233)

<400> 3
atg tct ccc gcc tgg ctc cgg ccc cga ctg cgg ttc tgt ctg ttc ctg 48
Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
1 5 10 15

ctg ctg ctg ctt ctg gtg ccg gcg gcg cgg ggc tgc ggg ccg ggc cgg 96
Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
20 25 30

gtg gtg ggc agc cgc cgg agg ccg cct cgc aag ctc gtg cct ctt gcc 144
Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
35 40 45

tac aag cag ttc agc ccc aac gtg ccg gag aag acc ctg ggc gcc agc 192
Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
50 55 60

ggg cgc tac gaa ggc aag atc gcg cgc agc tct gag cgc ttc aaa gag 240
Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
65 70 75 80

ctc acc ccc aac tac aat ccc gac atc atc ttc aag gac gag gag aac 288
Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
85 90 95

acg ggt gcc gac cgc ctc atg acc cag cgc tgc aag gac cgt ctg aac 336
Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
100 105 110

tca	ctg	gcc	atc	tct	gtc	atg	aac	cag	tgg	cct	ggg	gtg	aaa	ctg	cgg	384
Ser	Leu	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	
		115						120				125				
gtg	acc	gaa	ggc	cgg	gat	gaa	gat	ggc	cat	cac	tca	gag	gag	tct	tta	432
Val	Thr	Glu	Gly	Arg	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	
		130					135					140				
cac	tat	gag	ggc	cgc	gcg	gtg	gat	atc	acc	acc	tca	gac	cgt	gac	cga	480
His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	
		145				150				155					160	
aat	aag	tat	gga	ctg	ctg	gcg	cgc	tta	gca	gtg	gag	gcc	ggc	ttc	gac	528
Asn	Lys	Tyr	Gly	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	
				165					170					175		
tgg	gtg	tat	tac	gag	tcc	aag	gcc	cac	gtg	cat	tgc	tct	gtc	aag	tct	576
Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser	
			180					185					190			
gag	cat	tcg	gcc	gct	gcc	aag	aca	ggg	ggc	tgc	ttt	cct	gcc	gga	gcc	624
Glu	His	Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala	
		195					200					205				
cag	gtg	cgc	cta	gag	aac	ggg	gag	cgt	gtg	gcc	ctg	tca	gct	gta	aag	672
Gln	Val	Arg	Leu	Glu	Asn	Gly	Glu	Arg	Val	Ala	Leu	Ser	Ala	Val	Lys	
		210				215					220					
cca	gga	gac	cgg	gtg	ctg	gcc	atg	ggg	gag	gat	ggg	acc	ccc	acc	ttc	720
Pro	Gly	Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Thr	Pro	Thr	Phe	
		225				230				235					240	
agt	gat	gtg	ctt	att	ttc	ctg	gac	cgc	gag	cca	aac	cgg	ctg	aga	gct	768
Ser	Asp	Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	Asn	Arg	Leu	Arg	Ala	
				245					250					255		
ttc	cag	gtc	atc	gag	act	cag	gat	cct	ccg	cgt	cgg	ctg	gcg	ctc	acg	816
Phe	Gln	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	
			260					265					270			
cct	gcc	cac	ctg	ctc	ttc	att	gcg	gac	aat	cat	aca	gaa	cca	gca	gcc	864
Pro	Ala	His	Leu	Leu	Phe	Ile	Ala	Asp	Asn	His	Thr	Glu	Pro	Ala	Ala	
		275					280					285				
cac	ttc	cgg	gcc	aca	ttt	gcc	agc	cat	gtg	caa	cca	ggc	caa	tat	gtg	912
His	Phe	Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val	
		290				295					300					
ctg	gta	tca	ggg	gta	cca	ggc	ctc	cag	cct	gct	cgg	gtg	gca	gct	gtc	960
Leu	Val	Ser	Gly	Val	Pro	Gly	Leu	Gln	Pro	Ala	Arg	Val	Ala	Ala	Val	
		305				310				315					320	
tcc	acc	cac	gtg	gcc	ctt	ggg	tcc	tat	gct	cct	ctc	aca	agg	cat	ggg	1008
Ser	Thr	His	Val	Ala	Leu	Gly	Ser	Tyr	Ala	Pro	Leu	Thr	Arg	His	Gly	
				325					330					335		

aca ctt gtg gtg gag gat gtg gtg gcc tcc tgc ttt gca gct gtg gct 1056
 Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
 340 345 350

gac cac cat ctg gct cag ttg gcc ttc tgg ccc ctg cga ctg ttt ccc 1104
 Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro
 355 360 365

agt ttg gca tgg ggc agc tgg acc cca agt gag ggt gtt cac tcc tac 1152
 Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr
 370 375 380

cct cag atg ctc tac cgc ctg ggg cgt ctc ttg cta gaa gag agc acc 1200
 Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Ser Thr
 385 390 395 400

ttc cat cca ctg ggc atg tct ggg gca gga agc tgaagggact ctaaccactg 1253
 Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
 405 410

ccctcctgga actgctgtgc gtggatcc - 1281

<210> 4
 <211> 1313
 <212> DNA
 <213> Murine sp.

<220>
 <221> CDS
 <222> (1)..(1311)

<400> 4

atg ctg ctg ctg ctg gcc aga tgt ttt ctg gtg atc ctt gct tcc tgc 48
 Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser
 1 5 10 15

ctg ctg gtg tgc ccc ggg ctg gcc tgt ggg ccc ggc agg ggg ttt gga 96
 Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly
 20 25 30

aag agg cgg cac ccc aaa aag ctg acc cct tta gcc tac aag cag ttt 144
 Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe
 35 40 45

att ccc aac gta gcc gag aag acc cta ggg gcc agc ggc aga tat gaa 192
 Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu
 50 55 60

ggg aag atc aca aga aac tcc gaa cga ttt aag gaa ctc acc ccc aat 240
 Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn
 65 70 75 80

tac aac ccc gac atc ata ttt aag gat gag gaa aac acg gga gca gac 288
 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp
 85 90 95

cgg ctg atg act cag agg tgc aaa gac aag tta aat gcc ttg gcc atc	336
Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile	
100 105 110	
tct gtg atg aac cag tgg cct gga gtg agg ctg cga gtg acc gag ggc	384
Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly	
115 120 125	
tgg gat gag gac ggc cat cat tca gag gag tct cta cac tat gag ggt	432
Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly	
130 135 140	
cga gca gtg gac atc acc acg tcc gac cgg gac cgc agc aag tac ggc	480
Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly	
145 150 155 160	
atg ctg gct cgc ctg gct gtg gaa gca ggt ttc gac tgg gtc tac tat	528
Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr	
165 170 175	
gaa tcc aaa gct cac atc cac tgt tct gtg aaa gca gag aac tcc gtg	576
Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val	
180 185 190	
gcg gcc aaa tcc ggc ggc tgt ttc ccg gga tcc gcc acc gtg cac ctg	624
Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu	
195 200 205	
gag cag ggc ggc acc aag ctg gtg aag gac tta cgt ccc gga gac cgc	672
Glu Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Arg Pro Gly Asp Arg	
210 215 220	
gtg ctg gcg gct gac gac cag ggc cgg ctg ctg tac agc gac ttc ctc	720
Val Leu Ala Ala Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu	
225 230 235 240	
acc ttc ctg gac cgc gac gaa ggc gcc aag aag gtc ttc tac gtg atc	768
Thr Phe Leu Asp Arg Asp Glu Gly Ala Lys Lys Val Phe Tyr Val Ile	
245 250 255	
gag acg ctg gag ccg cgc gag cgc ctg ctg ctc acc gcc gcg cac ctg	816
Glu Thr Leu Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu	
260 265 270	
ctc ttc gtg gcg ccg cac aac gac tcg ggg ccc acg ccc ggg cca agc	864
Leu Phe Val Ala Pro His Asn Asp Ser Gly Pro Thr Pro Gly Pro Ser	
275 280 285	
gcg ctc ttt gcc agc cgc gtg cgc ccc ggg cag cgc gtg tac gtg gtg	912
Ala Leu Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val	
290 295 300	
gct gaa cgc ggc ggg gac cgc cgg ctg ctg ccc gcc gcg gtg cac agc	960
Ala Glu Arg Gly Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser	
305 310 315 320	

gtg acg ctg cga gag gag gag gcg ggc gcg tac gcg ccg ctc acg gcg	1008
Val Thr Leu Arg Glu Glu Glu Ala Gly Ala Tyr Ala Pro Leu Thr Ala	
325 330 335	
cac ggc acc att ctc atc aac cgg gtg ctc gcc tgc tgc tac gct gtc	1056
His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val	
340 345 350	
atc gag gag cac agc tgg gca cac cgg gcc ttc gcg cct ttc cgc ctg	1104
Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu	
355 360 365	
gcg cac gcg ctg ctg gcc gcg ctg gca ccc gcc cgc acg gac ggc ggg	1152
Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly	
370 375 380	
ggc ggg ggc agc atc cct gca gcg caa tct gca acg gaa gcg agg ggc	1200
Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly	
385 390 395 400	
gcg gag ccg act gcg ggc atc cac tgg tac tgc cag ctg ctc tac cac	1248
Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His	
405 410 415	
att ggc acc tgg ctg ttg gac agc gag acc atg cat ccc ttg gga atg	1296
Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met	
420 425 430	
gcg gtc aag tcc agc tg	1313
Ala Val Lys Ser Ser	
435	
<210> 5	
<211> 1256	
<212> DNA	
<213> Brachydanio rerio	
<220>	
<221> CDS	
<222> (1)..(1254)	
<400> 5	
atg cgg ctt ttg acg aga gtg ctg ctg gtg tct ctt ctc act ctg tcc	48
Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser	
1 5 10 15	
ttg gtg gtg tcc gga ctg gcc tgc ggt cct ggc aga ggc tac ggc aga	96
Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg	
20 25 30	
aga aga cat ccg aag aag ctg aca cct ctc gcc tac aag cag ttc ata	144
Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile	
35 40 45	
cct aat gtc gcg gag aag acc tta ggg gcc agc ggc aga tac gag ggc	192
Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly	
50 55 60	

aag	ata	acg	cgc	aat	tcg	gag	aga	ttt	aaa	gaa	ctt	act	cca	aat	tac	240
Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	
65					70					75					80	
aat	ccc	gac	att	atc	ttt	aag	gat	gag	gag	aac	acg	gga	gcg	gac	agg	288
Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg	
			85					90						95		
ctc	atg	aca	cag	aga	tgc	aaa	gac	aag	ctg	aac	tcg	ctg	gcc	atc	tct	336
Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ser	Leu	Ala	Ile	Ser	
			100					105					110			
gta	atg	aac	cac	tgg	cca	ggg	gtt	aag	ctg	cgt	gtg	aca	gag	ggc	tgg	384
Val	Met	Asn	His	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	Glu	Gly	Trp	
		115				120						125				
gat	gag	gac	ggt	cac	cat	ttt	gaa	gaa	tca	ctc	cac	tac	gag	gga	aga	432
Asp	Glu	Asp	Gly	His	His	Phe	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	
	130					135					140					
gct	gtt	gat	att	acc	acc	tct	gac	cga	gac	aag	agc	aaa	tac	ggg	aca	480
Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Lys	Ser	Lys	Tyr	Gly	Thr	
145					150					155					160	
ctg	tct	cgc	cta	gct	gtg	gag	gct	gga	ttt	gac	tgg	gtc	tat	tac	gag	528
Leu	Ser	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	
			165					170						175		
tcc	aaa	gcc	cac	att	cat	tgc	tct	gtc	aaa	gca	gaa	aat	tcg	gtt	gct	576
Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala	
		180						185					190			
gcg	aaa	tct	ggg	ggc	tgt	ttc	cca	ggt	tcg	gct	ctg	gtc	tcg	ctc	cag	624
Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Leu	Val	Ser	Leu	Gln	
		195					200					205				
gac	gga	gga	cag	aag	gcc	gtg	aag	gac	ctg	aac	ccc	gga	gac	aag	gtg	672
Asp	Gly	Gly	Gln	Lys	Ala	Val	Lys	Asp	Leu	Asn	Pro	Gly	Asp	Lys	Val	
	210					215					220					
ctg	gcg	gca	gac	agc	gcg	gga	aac	ctg	gtg	ttc	agc	gac	ttc	atc	atg	720
Leu	Ala	Ala	Asp	Ser	Ala	Gly	Asn	Leu	Val	Phe	Ser	Asp	Phe	Ile	Met	
225					230					235					240	
ttc	aca	gac	cga	gac	tcc	acg	acg	cga	cgt	gtg	ttt	tac	gtc	ata	gaa	768
Phe	Thr	Asp	Arg	Asp	Ser	Thr	Thr	Arg	Arg	Val	Phe	Tyr	Val	Ile	Glu	
			245					250						255		
acg	caa	gaa	ccc	gtt	gaa	aag	atc	acc	ctc	acc	gcc	gct	cac	ctc	ctt	816
Thr	Gln	Glu	Pro	Val	Glu	Lys	Ile	Thr	Leu	Thr	Ala	Ala	His	Leu	Leu	
			260					265					270			
ttt	gtc	ctc	gac	aac	tca	acg	gaa	gat	ctc	cac	acc	atg	acc	gcc	gcg	864
Phe	Val	Leu	Asp	Asn	Ser	Thr	Glu	Asp	Leu	His	Thr	Met	Thr	Ala	Ala	
		275					280					285				

tat gcc agc agt gtc aga gcc gga caa aag gtg atg gtt gtt gat gat	912
Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp	
290 295 300	
agc ggt cag ctt aaa tct gtc atc gtg cag cgg ata tac acg gag gag	960
Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu	
305 310 315 320	
cag cgg ggc tcg ttc gca cca gtg act gca cat ggg acc att gtg gtc	1008
Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val	
325 330 335	
gac aga ata ctg gcg tcc tgt tac gcc gta ata gag gac cag ggg ctt	1056
Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu	
340 345 350	
gcg cat ttg gcc ttc gcg ccc gcc agg ctc tat tat tac gtg tca tca	1104
Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser	
355 360 365	
ttc ctg tcc ccc aaa act cca gca gtc ggt cca atg cga ctt tac aac	1152
Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn	
370 375 380	
agg agg ggg tcc act ggt act cca ggc tcc tgt cat caa atg gga acg	1200
Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr	
385 390 395 400	
tgg ctt ttg gac agc aac atg ctt cat cct ttg ggg atg tca gta aac	1248
Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn	
405 410 415	
tca agc tg	1256
Ser Ser	
<210> 6	
<211> 1425	
<212> DNA	
<213> Homo sapien	
<220>	
<221> CDS	
<222> (1)..(1425)	
<220>	
<221> MOD_RES	
<222> (1397)..(1389)	
<223> a, t, c, g, other or unknown	
<400> 6	
atg ctg ctg ctg gcg aga tgt ctg ctg cta gtc ctc gtc tcc tcg ctg	48
Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu	
1 5 10 15	
ctg gta tgc tcg gga ctg gcg tgc gga ccg ggc agg ggg ttc ggg aag	96
Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys	
20 25 30	

agg agg cac ccc aaa aag ctg acc cct tta gcc tac aag cag ttt atc	144
Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile	
35 40 45	
ccc aat gtg gcc gag aag acc cta ggc gcc agc gga agg tat gaa ggg	192
Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly	
50 55 60	
aag atc tcc aga aac tcc gag cga ttt aag gaa ctc acc ccc aat tac	240
Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr	
65 70 75 80	
aac ccc gac atc ata ttt aag gat gaa gaa aac acc gga gcg gac agg	288
Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg	
85 90 95	
ctg atg act cag agg tgt aag gac aag ttg aac gct ttg gcc atc tcg	336
Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser	
100 105 110	
gtg atg aac cag tgg cca gga gtg aaa ctg cgg gtg acc gag ggc tgg	384
Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp	
115 120 125	
gac gaa gat ggc cac cac tca gag gag tct ctg cac tac gag ggc cgc	432
Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg	
130 135 140	
gca gtg gac atc acc acg tct gac cgc gac cgc agc aag tac ggc atg	480
Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met	
145 150 155 160	
ctg gcc cgc ctg gcg gtg gag gcc ggc ttc gac tgg gtg tac tac gag	528
Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu	
165 170 175	
tcc aag gca cat atc cac tgc tgc gtg aaa gca gag aac tcg gtg gcg	576
Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala	
180 185 190	
gcc aaa tcg gga ggc tgc ttc ccg ggc tcg gcc acg gtg cac ctg gag	624
Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu	
195 200 205	
cag ggc ggc acc aag ctg gtg aag gac ctg agc ccc ggg gac cgc gtg	672
Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly Asp Arg Val	
210 215 220	
ctg gcg gcg gac gac cag ggc cgg ctg ctc tac agc gac ttc ctc act	720
Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu Thr	
225 230 235 240	
ttc ctg gac cgc gac gac ggc gcc aag aag gtc ttc tac gtg atc gag	768
Phe Leu Asp Arg Asp Asp Gly Ala Lys Lys Val Phe Tyr Val Ile Glu	
245 250 255	

acg cgg gag ccg cgc gag cgc ctg ctg ctc acc gcc gcg cac ctg ctc	816
Thr Arg Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu Leu	
260 265 270	
ttt gtg gcg ccg cac aac gac tcg gcc acc ggg gag ccc gag gcg tcc	864
Phe Val Ala Pro His Asn Asp Ser Ala Thr Gly Glu Pro Glu Ala Ser	
275 280 285	
tcg ggc tcg ggg ccg cct tcc ggg ggc gca ctg ggg cct cgg gcg ctg	912
Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu	
290 295 300	
ttc gcc agc cgc gtg cgc ccg ggc cag cgc gtg tac gtg gtg gcc gag	960
Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu	
305 310 315 320	
cgt gac ggg gac cgc cgg ctc ctg ccc gcc gct gtg cac agc gtg acc	1008
Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr	
325 330 335	
cta agc gag gag gcc gcg ggc gcc tac gcg ccg ctc acg gcc cag ggc	1056
Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly	
340 345 350	
acc att ctc atc aac cgg gtg ctg gcc tcg tgc tac gcg gtc atc gag	1104
Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu	
355 360 365	
gag cac agc tgg gcg cac cgg gcc ttc gcg ccc ttc cgc ctg gcg cac	1152
Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His	
370 375 380	
gcg ctc ctg gct gca ctg gcg ccc gcg cgc acg gac cgc ggc ggg gac	1200
Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp	
385 390 395 400	
agc ggc ggc ggg gac cgc ggg ggc ggc ggc ggc aga gta gcc cta acc	1248
Ser Gly Gly Gly Asp Arg Gly Gly Gly Gly Gly Arg Val Ala Leu Thr	
405 410 415	
gct cca ggt gct gcc gac gct ccg ggt gcg ggg gcc acc gcg ggc atc	1296
Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile	
420 425 430	
cac tgg tac tcg cag ctg ctc tac caa ata ggc acc tgg ctc ctg gac	1344
His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp	
435 440 445	
agc gag gcc ctg cac ccg ctg ggc atg gcg gtc aag tcc agc nnn agc	1392
Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser	
450 455 460	
cgg ggg gcc ggg gga ggg gcg cgg gag ggg gcc	1425
Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala	
465 470 475	

<210> 7

<211> 1622

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (51)..(1283)

<400> 7

```

catcagccca ccaggagacc tcgcccgcgcg ctcccccgagg ctcccccgagg atg tct      56
                                   Met Ser
                                   1

ccc gcc cgg ctc cgg ccc cga ctg cac ttc tgc ctg gtc ctg ttg ctg      104
Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu Leu Leu
      5                      10                      15

ctg ctg gtg gtg ccc gcg gca tgg ggc tgc ggg ccg ggt cgg gtg gtg      152
Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg Val Val
      20                      25                      30

ggc agc cgc cgg cga ccg cca cgc aaa ctc gtg ccg ctc gcc tac aag      200
Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala Tyr Lys
      35                      40                      45                      50

cag ttc agc ccc aat gtg ccc gag aag acc ctg ggc gcc agc gga cgc      248
Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser Gly Arg
      55                      60                      65

tat gaa ggc aag atc gct cgc agc tcc gag cgc ttc aag gag ctc acc      296
Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu Leu Thr
      70                      75                      80

ccc aat tac aat cca gac atc atc ttc aag gac gag gag aac aca ggc      344
Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
      85                      90                      95

gcc gac cgc ctc atg acc cag cgc tgc aag gac cgc ctg aac tcg ctg      392
Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn Ser Leu
      100                      105                      110

gct atc tcg gtg atg aac cag tgg ccc ggt gtg aag ctg cgg gtg acc      440
Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
      115                      120                      125                      130

gag ggc tgg gac gag gac ggc cac cac tca gag gag tcc ctg cat tat      488
Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
      135                      140                      145

gag ggc cgc gcg gtg gac atc acc aca tca gac cgc gac cgc aat aag      536
Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys
      150                      155                      160

tat gga ctg ctg gcg cgc ttg gca gtg gag gcc ggc ttt gac tgg gtg      584
Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
      165                      170                      175

```

tat	tac	gag	tca	aag	gcc	cac	gtg	cat	tgc	tcc	gtc	aag	tcc	gag	cac	632
Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser	Glu	His	
180						185					190					
tcg	gcc	gca	gcc	aag	acg	ggc	ggc	tgc	ttc	cct	gcc	gga	gcc	cag	gta	680
Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala	Gln	Val	
195					200					205					210	
cgc	ctg	gag	agt	ggg	gcg	cgt	gtg	gcc	ttg	tca	gcc	gtg	agg	ccg	gga	728
Arg	Leu	Glu	Ser	Gly	Ala	Arg	Val	Ala	Leu	Ser	Ala	Val	Arg	Pro	Gly	
				215					220					225		
gac	cgt	gtg	ctg	gcc	atg	ggg	gag	gat	ggg	agc	ccc	acc	ttc	agc	gat	776
Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Ser	Pro	Thr	Phe	Ser	Asp	
			230					235						240		
gtg	ctc	att	ttc	ctg	gac	cgc	gag	ccc	cac	agg	ctg	aga	gcc	ttc	cag	824
Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	His	Arg	Leu	Arg	Ala	Phe	Gln	
		245					250					255				
gtc	atc	gag	act	cag	gac	ccc	cca	cgc	cgc	ctg	gca	ctc	aca	ccc	gct	872
Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	Pro	Ala	
	260					265					270					
cac	ctg	ctc	ttt	acg	gct	gac	aat	cac	acg	gag	ccg	gca	gcc	cgc	ttc	920
His	Leu	Leu	Phe	Thr	Ala	Asp	Asn	His	Thr	Glu	Pro	Ala	Ala	Arg	Phe	
275					280					285					290	
cgg	gcc	aca	ttt	gcc	agc	cac	gtg	cag	cct	ggc	cag	tac	gtg	ctg	gtg	968
Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val	Leu	Val	
				295					300					305		
gct	ggg	gtg	cca	ggc	ctg	cag	cct	gcc	cgc	gtg	gca	gct	gtc	tct	aca	1016
Ala	Gly	Val	Pro	Gly	Leu	Gln	Pro	Ala	Arg	Val	Ala	Ala	Val	Ser	Thr	
			310					315						320		
cac	gtg	gcc	ctc	ggg	gcc	tac	gcc	ccg	ctc	aca	aag	cat	ggg	aca	ctg	1064
His	Val	Ala	Leu	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Lys	His	Gly	Thr	Leu	
		325					330					335				
gtg	gtg	gag	gat	gtg	gtg	gca	tcc	tgc	ttc	gcg	gcc	gtg	gct	gac	cac	1112
Val	Val	Glu	Asp	Val	Val	Ala	Ser	Cys	Phe	Ala	Ala	Val	Ala	Asp	His	
	340					345					350					
cac	ctg	gct	cag	ttg	gcc	ttc	tgg	ccc	ctg	aga	ctc	ttt	cac	agc	ttg	1160
His	Leu	Ala	Gln	Leu	Ala	Phe	Trp	Pro	Leu	Arg	Leu	Phe	His	Ser	Leu	
355					360					365					370	
gca	tgg	ggc	agc	tgg	acc	ccg	ggg	gag	ggt	gtg	cat	tgg	tac	ccc	cag	1208
Ala	Trp	Gly	Ser	Trp	Thr	Pro	Gly	Glu	Gly	Val	His	Trp	Tyr	Pro	Gln	
				375				380						385		
ctg	ctc	tac	cgc	ctg	ggg	cgt	ctc	ctg	cta	gaa	gag	ggc	agc	ttc	cac	1256
Leu	Leu	Tyr	Arg	Leu	Gly	Arg	Leu	Leu	Leu	Glu	Glu	Gly	Ser	Phe	His	
			390					395						400		

cca ctg ggc atg tcc ggg gca ggg agc tgaaaggact ccaccgctgc 1303
 Pro Leu Gly Met Ser Gly Ala Gly Ser
 405 410

cctcctggaa ctgctgtact ggggtccagaa gcctctcagc caggagggag ctggccctgg 1363
 aagggaacctg agctggggga cactggctcc tgccatctcc tctgccatga agatacacca 1423
 ttgagacttg actgggcaac accagcgtcc cccacccgag tctgggtgta gtcatagagc 1483
 tgcaagctga gctggcgagg ggatggttgt tgacccctct ctctagaga ccttgaggct 1543
 ggcacggcga ctcccaactc agcctgctct cactacgagt ttccatactc tgccctcccc 1603
 attgggaggg cccattccc 1622

<210> 8

<211> 1190

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (1)..(1188)

<400> 8

atg gct ctc ctg acc aat cta ctg ccc ttg tgc tgc ttg gca ctt ctg 48
 Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
 1 5 10 15

gcg ctg cca gcc cag agc tgc ggg ccg ggc cgg ggg ccg gtt ggc cgg 96
 Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
 20 25 30

cgc cgc tat gcg cgc aag cag ctc gtg ccg cta ctc tac aag caa ttt 144
 Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
 35 40 45

gtg ccc ggc gtg cca gag cgg acc ctg ggc gcc agt ggg cca gcg gag 192
 Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
 50 55 60

ggg agg gtg gca agg ggc tcc gag cgc ttc cgg gac ctc gtg ccc aac 240
 Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
 65 70 75 80

tac aac ccc gac atc atc ttc aag gat gag gag aac agt gga gcc gac 288
 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
 85 90 95

cgc ctg atg acc gag cgt tgc aag gag agg gtg aac gct ttg gcc att 336
 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
 100 105 110

gcc gtg atg aac atg tgg ccc gga gtg cgc cta cga gtg act gag ggc 384
 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
 115 120 125

tgg gac gag gac ggc cac cac gct cag gat tca ctc cac tac gaa ggc	432
Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly	
130 135 140	
cgt gct ttg gac atc act acg tct gac cgc gac cgc aac aag tat ggg	480
Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly	
145 150 155 160	
ttg ctg gcg cgc ctc gca gtg gaa gcc ggc ttc gac tgg gtc tac tac	528
Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr	
165 170 175	
gag tcc cgc aac cac gtc cac gtg tcg gtc aaa gct gat aac tca ctg	576
Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu	
180 185 190	
gcg gtc cgg gcg ggc ggc tgc ttt ccg gga aat gca act gtg cgc ctg	624
Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu	
195 200 205	
tgg agc ggc gag cgg aaa ggg ctg cgg gaa ctg cac cgc gga gac tgg	672
Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp	
210 215 220	
gtt ttg gcg gcc gat gcg tca ggc cgg gtg gtg ccc acg ccg gtg ctg	720
Val Leu Ala Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu	
225 230 235 240	
ctc ttc ctg gac cgg gac ttg cag cgc cgg gct tca ttt gtg gct gtg	768
Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val	
245 250 255	
gag acc gag tgg cct cca cgc aaa ctg ttg ctc acg ccc tgg cac ctg	816
Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu	
260 265 270	
gtg ttt gcc gct cga ggg ccg gcg ccc gcg cca ggc gac ttt gca ccg	864
Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro	
275 280 285	
gtg ttc gcg cgc cgg cta cgc gct ggg gac tcg gtg ctg gcg ccc ggc	912
Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly	
290 295 300	
ggg gat gcg ctt cgg cca gcg cgc gtg gcc cgt gtg gcg cgg gag gaa	960
Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu	
305 310 315 320	
gcc gtg ggc gtg ttc gcg ccg ctc acc gcg cac ggg acg ctg ctg gtg	1008
Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val	
325 330 335	
aac gat gtc ctg gcc tct tgc tac gcg gtt ctg gag agt cac cag tgg	1056
Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp	
340 345 350	

gcg cac cgc gct ttt gcc ccc ttg aga ctg ctg cac gcg cta ggg gcg 1104
 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
 355 360 365

ctg ctc ccc ggc ggg gcc gtc cag ccg act ggc atg cat tgg tac tct 1152
 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
 370 375 380

cgg ctc ctc tac cgc tta gcg gag gag cta ctg ggc tg 1190
 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly
 385 390 395

<210> 9
 <211> 1251
 <212> DNA
 <213> Brachydanio rerio

<220>
 <221> CDS
 <222> (1)..(1248)

<400> 9

atg gac gta agg ctg cat ctg aag caa ttt gct tta ctg tgt ttt atc 48
 Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile
 1 5 10 15

agc ttg ctt ctg acg cct tgt gga tta gcc tgt ggt cct ggt aga ggt 96
 Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly
 20 25 30

tat gga aaa cga aga cac cca aag aaa tta acc ccg ttg gct tac aag 144
 Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
 35 40 45

caa ttc atc ccc aac gtt gct gag aaa acg ctt gga gcc agc ggc aaa 192
 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys
 50 55 60

tac gaa ggc aaa atc aca agg aat tca gag aga ttt aaa gag ctg att 240
 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile
 65 70 75 80

ccg aat tat aat ccc gat atc atc ttt aag gac gag gaa aac aca aac 288
 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn
 85 90 95

gct gac agg ctg atg acc aag cgc tgt aag gac aag tta aat tcg ttg 336
 Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu
 100 105 110

gcc ata tcc gtc atg aac cac tgg ccc ggc gtg aaa ctg cgc gtc act 384
 Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr
 115 120 125

gaa ggc tgg gat gag gat ggt cac cat tta gaa gaa tct ttg cac tat 432
 Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr
 130 135 140

gag gga cgg gca gtg gac atc act acc tca gac agg gat aaa agc aag	480
Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys	
145 150 155 160	
tat ggg atg cta tcc agg ctt gca gtg gag gca gga ttc gac tgg gtc	528
Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val	
165 170 175	
tat tat gaa tct aaa gcc cac ata cac tgc tct gtc aaa gca gaa aat	576
Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn	
180 185 190	
tca gtg gct gct aaa tca gga gga tgt ttt cct ggg tct ggg acg gtg	624
Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val	
195 200 205	
aca ctt ggt gat ggg acg agg aaa ccc atc aaa gat ctt aaa gtg ggc	672
Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly	
210 215 220	
gac cgg gtt ttg gct gca gac gag aag gga aat gtc tta ata agc gac	720
Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp	
225 230 235 240	
ttt att atg ttt ata gac cac gat ccg aca acg aga agg caa ttc atc	768
Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile	
245 250 255	
gtc atc gag acg tca gaa cct ttc acc aag ctc acc ctc act gcc gcg	816
Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala	
260 265 270	
cac cta gtt ttc gtt gga aac tct tca gca gct tcg ggt ata aca gca	864
His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala	
275 280 285	
aca ttt gcc agc aac gtg aag cct gga gat aca gtt tta gtg tgg gaa	912
Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu	
290 295 300	
gac aca tgc gag agc ctc aag agc gtt aca gtg aaa agg att tac act	960
Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr	
305 310 315 320	
gag gag cac gag ggc tct ttt gcg cca gtc acc gcg cac gga acc ata	1008
Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile	
325 330 335	
ata gtg gat cag gtg ttg gca tcg tgc tac gcg gtc att gag aac cac	1056
Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His	
340 345 350	
aaa tgg gca cat tgg gct ttt gcg ccg gtc agg ttg tgt cac aag ctg	1104
Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu	
355 360 365	

atg acg tgg ctt ttt ccg gct cgt gaa tca aac gtc aat ttt cag gag 1152
 Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu
 370 375 380

gat ggt atc cac tgg tac tca aat atg ctg ttt cac atc ggc tct tgg 1200
 Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp
 385 390 395 400

ctg ctg gac aga gac tct ttc cat cca ctc ggg att tta cac tta agt 1248
 Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser
 405 410 415

tga 1251

<210> 10

<211> 425

<212> PRT

<213> Gallus sp.

<400> 10

Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
 1 5 10 15

Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
 20 25 30

Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
 35 40 45

Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
 50 55 60

Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
 65 70 75 80

Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
 85 90 95

Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
 100 105 110

Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
 115 120 125

Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
 130 135 140

Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys
 145 150 155 160

Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
 165 170 175

Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
 180 185 190

Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val
 195 200 205

His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly
210 215 220

Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp
225 230 235 240

Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
245 250 255

Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala
260 265 270

His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
275 280 285

Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
290 295 300

Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser
305 310 315 320

Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
325 330 335

Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
340 345 350

Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
355 360 365

Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
370 375 380

Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
385 390 395 400

Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
405 410 415

Pro Leu Gly Met Val Ala Pro Ala Ser
420 425

<210> 11

<211> 396

<212> PRT

<213> Murine sp.

<400> 11

Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
1 5 10 15

Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
20 25 30

Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
35 40 45

Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
 50 55 60
 Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
 65 70 75 80
 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
 85 90 95
 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
 100 105 110
 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
 115 120 125
 Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
 130 135 140
 Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
 145 150 155 160
 Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
 165 170 175
 Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
 180 185 190
 Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
 195 200 205
 Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
 210 215 220
 Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu
 225 230 235 240
 Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
 245 250 255
 Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
 260 265 270
 Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
 275 280 285
 Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
 290 295 300
 Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
 305 310 315 320
 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
 325 330 335
 Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
 340 345 350

Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
 355 360 365

Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
 370 375 380

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
 385 390 395

<210> 12

<211> 411

<212> PRT

<213> Murine sp.

<400> 12

Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
 1 5 10 15

Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
 20 25 30

Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
 35 40 45

Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
 50 55 60

Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
 65 70 75 80

Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
 85 90 95

Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
 100 105 110

Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
 115 120 125

Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
 130 135 140

His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
 145 150 155 160

Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
 165 170 175

Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
 180 185 190

Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
 195 200 205

Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys
 210 215 220

Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe
225 230 235 240

Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala
245 250 255

Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
260 265 270

Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala
275 280 285

His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val
290 295 300

Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val
305 310 315 320

Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly
325 330 335

Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
340 345 350

Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro
355 360 365

Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr
370 375 380

Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Ser Thr
385 390 395 400

Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
405 410

<210> 13

<211> 437

<212> PRT

<213> Murine sp.

<400> 13

Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser
1 5 10 15

Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly
20 25 30

Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe
35 40 45

Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu
50 55 60

Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn
65 70 75 80

Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp
 85 90 95
 Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile
 100 105 110
 Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
 115 120 125
 Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly
 130 135 140
 Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly
 145 150 155 160
 Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
 165 170 175
 Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val
 180 185 190
 Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu
 195 200 205
 Glu Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Arg Pro Gly Asp Arg
 210 215 220
 Val Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu
 225 230 235 240
 Thr Phe Leu Asp Arg Asp Glu Gly Ala Lys Lys Val Phe Tyr Val Ile
 245 250 255
 Glu Thr Leu Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu
 260 265 270
 Leu Phe Val Ala Pro His Asn Asp Ser Gly Pro Thr Pro Gly Pro Ser
 275 280 285
 Ala Leu Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val
 290 295 300
 Ala Glu Arg Gly Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser
 305 310 315 320
 Val Thr Leu Arg Glu Glu Glu Ala Gly Ala Tyr Ala Pro Leu Thr Ala
 325 330 335
 His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val
 340 345 350
 Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu
 355 360 365
 Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly
 370 375 380

Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly
385 390 395 400

Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His
405 410 415

Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met
420 425 430

Ala Val Lys Ser Ser
435

<210> 14

<211> 418

<212> PRT

<213> Brachydanio rerio

<400> 14

Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser
1 5 10 15

Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg
20 25 30

Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
35 40 45

Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
50 55 60

Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
65 70 75 80

Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
85 90 95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser
100 105 110

Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
115 120 125

Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg
130 135 140

Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr
145 150 155 160

Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
165 170 175

Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
180 185 190

Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln
195 200 205

Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val
 210 215 220
 Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met
 225 230 235 240
 Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu
 245 250 255
 Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu
 260 265 270
 Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala
 275 280 285
 Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp
 290 295 300
 Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu
 305 310 315 320
 Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val
 325 330 335
 Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu
 340 345 350
 Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser
 355 360 365
 Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn
 370 375 380
 Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr
 385 390 395 400
 Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn
 405 410 415

Ser Ser

<210> 15

<211> 475

<212> PRT

<213> Homo sapien

<220>

<221> MOD_RES

<222> (463)

<223> any or unknown amino acid

<400> 15

Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu
 1 5 10 15

Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys
 20 25 30

Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
 35 40 45
 Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
 50 55 60
 Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
 65 70 75 80
 Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
 85 90 95
 Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser
 100 105 110
 Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
 115 120 125
 Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg
 130 135 140
 Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met
 145 150 155 160
 Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
 165 170 175
 Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
 180 185 190
 Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu
 195 200 205
 Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly Asp Arg Val
 210 215 220
 Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu Thr
 225 230 235 240
 Phe Leu Asp Arg Asp Asp Gly Ala Lys Lys Val Phe Tyr Val Ile Glu
 245 250 255
 Thr Arg Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu Leu
 260 265 270
 Phe Val Ala Pro His Asn Asp Ser Ala Thr Gly Glu Pro Glu Ala Ser
 275 280 285
 Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu
 290 295 300
 Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu
 305 310 315 320
 Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr
 325 330 335

Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly
 340 345 350
 Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu
 355 360 365
 Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His
 370 375 380
 Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp
 385 390 395 400
 Ser Gly Gly Gly Asp Arg Gly Gly Gly Gly Gly Arg Val Ala Leu Thr
 405 410 415
 Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile
 420 425 430
 His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp
 435 440 445
 Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser
 450 455 460
 Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala
 465 470 475

<210> 16

<211> 411

<212> PRT

<213> Homo sapien

<400> 16

Met Ser Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu
 1 5 10 15
 Leu Leu Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg
 20 25 30
 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
 35 40 45
 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
 50 55 60
 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
 65 70 75 80
 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
 85 90 95
 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
 100 105 110
 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
 115 120 125

Val	Thr	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu
130						135					140				
His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg
145					150					155					160
Asn	Lys	Tyr	Gly	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp
			165						170					175	
Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser
			180					185					190		
Glu	His	Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala
		195					200					205			
Gln	Val	Arg	Leu	Glu	Ser	Gly	Ala	Arg	Val	Ala	Leu	Ser	Ala	Val	Arg
	210					215					220				
Pro	Gly	Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Ser	Pro	Thr	Phe
225					230					235					240
Ser	Asp	Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	His	Arg	Leu	Arg	Ala
			245						250					255	
Phe	Gln	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr
		260					265						270		
Pro	Ala	His	Leu	Leu	Phe	Thr	Ala	Asp	Asn	His	Thr	Glu	Pro	Ala	Ala
		275					280					285			
Arg	Phe	Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val
	290					295					300				
Leu	Val	Ala	Gly	Val	Pro	Gly	Leu	Gln	Pro	Ala	Arg	Val	Ala	Ala	Val
305					310					315					320
Ser	Thr	His	Val	Ala	Leu	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Lys	His	Gly
			325						330					335	
Thr	Leu	Val	Val	Glu	Asp	Val	Val	Ala	Ser	Cys	Phe	Ala	Ala	Val	Ala
		340						345					350		
Asp	His	His	Leu	Ala	Gln	Leu	Ala	Phe	Trp	Pro	Leu	Arg	Leu	Phe	His
		355					360					365			
Ser	Leu	Ala	Trp	Gly	Ser	Trp	Thr	Pro	Gly	Glu	Gly	Val	His	Trp	Tyr
	370					375					380				
Pro	Gln	Leu	Leu	Tyr	Arg	Leu	Gly	Arg	Leu	Leu	Leu	Glu	Glu	Gly	Ser
385					390					395					400
Phe	His	Pro	Leu	Gly	Met	Ser	Gly	Ala	Gly	Ser					
			405						410						

<210> 17

<211> 396

<212> PRT

<213> Homo sapien

<400> 17

Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
 1 5 10 15
 Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
 20 25 30
 Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
 35 40 45
 Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
 50 55 60
 Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
 65 70 75 80
 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
 85 90 95
 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
 100 105 110
 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
 115 120 125
 Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
 130 135 140
 Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
 145 150 155 160
 Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
 165 170 175
 Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu
 180 185 190
 Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
 195 200 205
 Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
 210 215 220
 Val Leu Ala Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu
 225 230 235 240
 Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
 245 250 255
 Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
 260 265 270
 Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
 275 280 285
 Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
 290 295 300

Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
305 310 315 320

Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
325 330 335

Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
340 345 350

Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
355 360 365

Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
370 375 380

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly
385 390 395

<210> 18

<211> 416

<212> PRT

<213> Brachydanio rerio

<400> 18

Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile
1 5 10 15

Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly
20 25 30

Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
35 40 45

Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys
50 55 60

Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile
65 70 75 80

Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn
85 90 95

Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu
100 105 110

Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr
115 120 125

Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr
130 135 140

Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys
145 150 155 160

Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
165 170 175

Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
 180 185 190

Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val
 195 200 205

Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly
 210 215 220

Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp
 225 230 235 240

Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile
 245 250 255

Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala
 260 265 270

His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala
 275 280 285

Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu
 290 295 300

Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr
 305 310 315 320

Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile
 325 330 335

Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His
 340 345 350

Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu
 355 360 365

Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu
 370 375 380

Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp
 385 390 395 400

Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser
 405 410 415

<210> 19

<211> 1416

<212> DNA

<213> Drosophila sp.

<220>

<221> CDS

<222> (1)...(1413)

<400> 19

atg gat aac cac agc tca gtg cct tgg gcc agt gcc gcc agt gtc acc
 Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr
 1 5 10 15

48

tgt ctc tcc ctg gga tgc caa atg cca cag ttc cag ttc cag ttc cag	96
Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln Phe Gln	
20 25 30	
ctc caa atc cgc agc gag ctc cat ctc cgc aag ccc gca aga aga acg	144
Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr	
35 40 45	
caa acg atg cgc cac att gcg cat acg cag cgt tgc ctc agc agg ctg	192
Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu	
50 55 60	
acc tct ctg gtg gcc ctg ctg ctg atc gtc ttg ccg atg gtc ttt agc	240
Thr Ser Leu Val Ala Leu Leu Leu Ile Val Leu Pro Met Val Phe Ser	
65 70 75 80	
ccg gct cac agc tgc ggt cct ggc cga gga ttg ggt cgt cat agg gcg	288
Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala	
85 90 95	
cgc aac ctg tat ccg ctg gtc ctc aag cag aca att ccc aat cta tcc	336
Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser	
100 105 110	
gag tac acg aac agc gcc tcc gga cct ctg gag ggt gtg atc cgt cgg	384
Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg	
115 120 125	
gat tgc ccc aaa ttc aag gac ctc gtg ccc aac tac aac agg gac atc	432
Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile	
130 135 140	
ctt ttc cgt gac gag gaa ggc acc gga gcg gat ggc ttg atg agc aag	480
Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys	
145 150 155 160	
cgc tgc aag gag aag cta aac gtg ctg gcc tac tgc gtg atg aac gaa	528
Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu	
165 170 175	
tgg ccc ggc atc cgg ctg ctg gtc acc gag agc tgg gac gag gac tac	576
Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr	
180 185 190	
cat cac ggc cag gag tgc ctc cac tac gag ggc cga gcg gtg acc att	624
His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile	
195 200 205	
gcc acc tcc gat cgc gac cag tcc aaa tac ggc atg ctc gct cgc ctg	672
Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu	
210 215 220	
gcc gtc gag gct gga ttc gat tgg gtc tcc tac gtc agc agg cgc cac	720
Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His	
225 230 235 240	

atc tac tgc tcc gtc aag tca gat tgc tgc atc agt tcc cac gtg cac	768
Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His	
245 250 255	
ggc tgc ttc acg ccg gag agc aca gcg ctg ctg gag agt gga gtc cgg	816
Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg	
260 265 270	
aag ccg ctc ggc gag ctc tct atc gga gat cgt gtt ttg agc atg acc	864
Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr	
275 280 285	
gcc aac gga cag gcc gtc tac agc gaa gtg atc ctc ttc atg gac cgc	912
Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg	
290 295 300	
aac ctc gag cag atg caa aac ttt gtg cag ctg cac acg gac ggt gga	960
Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly	
305 310 315 320	
gca gtg ctc acg gtg acg ccg gct cac ctg gtt agc gtt tgg cag ccg	1008
Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro	
325 330 335	
gag agc cag aag ctc acg ttt gtg ttt gcg cat cgc atc gag gag aag	1056
Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys	
340 345 350	
aac cag gtg ctc gta cgg gat gtg gag acg ggc gag ctg agg ccc cag	1104
Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln	
355 360 365	
cga gtg gtc aag ttg ggc agt gtg cgc agt aag ggc gtg gtc gcg ccg	1152
Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro	
370 375 380	
ctg acc cgc gag ggc acc att gtg gtc aac tgc gtg gcc gcc agt tgc	1200
Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys	
385 390 395 400	
tat gcg gtg atc aac agt cag tgc ctg gcc cac tgg gga ctg gct ccc	1248
Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro	
405 410 415	
atg cgc ctg ctg tcc acg ctg gag gcg tgg ctg ccc gcc aag gag cag	1296
Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln	
420 425 430	
ttg cac agt tgc ccg aag gtg gtg agc tgc gcg cag cag cag aat ggc	1344
Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly	
435 440 445	
atc cat tgg tat gcc aat gcg ctc tac aag gtc aag gac tac gtg ctg	1392
Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu	
450 455 460	

ccg cag agc tgg cgc cac gat tga
 Pro Gln Ser Trp Arg His Asp
 465 470

1416

<210> 20
 <211> 471
 <212> PRT
 <213> Drosophila sp.

<400> 20
 Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr
 1 5 10 15
 Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln Phe Gln
 20 25 30
 Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr
 35 40 45
 Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu
 50 55 60
 Thr Ser Leu Val Ala Leu Leu Leu Ile Val Leu Pro Met Val Phe Ser
 65 70 75 80
 Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala
 85 90 95
 Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser
 100 105 110
 Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg
 115 120 125
 Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile
 130 135 140
 Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys
 145 150 155 160
 Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu
 165 170 175
 Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr
 180 185 190
 His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile
 195 200 205
 Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu
 210 215 220
 Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His
 225 230 235 240
 Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His
 245 250 255

Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg
 260 265 270
 Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr
 275 280 285
 Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg
 290 295 300
 Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly
 305 310 315 320
 Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro
 325 330 335
 Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys
 340 345 350
 Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln
 355 360 365
 Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro
 370 375 380
 Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys
 385 390 395 400
 Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro
 405 410 415
 Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln
 420 425 430
 Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly
 435 440 445
 Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu
 450 455 460
 Pro Gln Ser Trp Arg His Asp
 465 470

<210> 21

<211> 221

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: degenerate polypeptide sequence

<220>

<221> MOD_RES

<222> 7

<223> Gly, Ala, Val, Leu, Ile, Phe, Tyr or Trp

<220>
<221> MOD_RES
<222> 9
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 44
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 85
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 93
<223> Lys, Arg, His, Asn or Gln

<220>
<221> MOD_RES
<222> 98
<223> Lys, Arg or His

<220>
<221> MOD_RES
<222> 112
<223> Ser, Thr, Tyr, Trp or Phe

<220>
<221> MOD_RES
<222> 132
<223> Lys, Arg or His

<220>
<221> MOD_RES
<222> 137
<223> Met, Cys, Ser or Thr

<220>
<221> MOD_RES
<222> 139
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 181
<223> Leu, Val, Met, Thr or Ser

<220>
<221> MOD_RES
<222> 183
<223> His, Phe, Tyr, Ser, Thr, Met or Cys

<220>
<221> MOD_RES
<222> 185

<223> Gln, Asn, Glu, or Asp

<220>

<221> MOD_RES

<222> 186

<223> His, Phe, Tyr, Thr, Gln, Asn, Glu or Asp

<220>

<221> MOD_RES

<222> 189

<223> Gln, Asn, Glu, Asp, Thr, Ser, Met or Cys

<220>

<221> MOD_RES

<222> 191

<223> Ala, Gly, Cys, Leu, Val or Met

<220>

<221> MOD_RES

<222> 196

<223> Arg, Lys, Met, Ile, Asn, Asp, Glu, Gln, Ser, Thr or Cys

<220>

<221> MOD_RES

<222> 200

<223> Arg, Lys, Met or Ile

<220>

<221> MOD_RES

<222> 206

<223> Ala, Gly, Cys, Asp, Glu, Gln, Asn, Ser, Thr or Met

<220>

<221> MOD_RES

<222> 207

<223> Ala, Gly, Cys, Asp, Asn, Glu or Gln

<220>

<221> MOD_RES

<222> 209

<223> Arg, Lys, Met, Ile, Asn, Asp, Glu or Gln

<220>

<221> MOD_RES

<222> 211

<223> Leu, Val, Met or Ile

<220>

<221> MOD_RES

<222> 212

<223> Phe, Tyr, Thr, His or Trp

<220>

<221> MOD_RES

<222> 216

<223> Ile, Val, Leu or Met

<220>

<221> MOD_RES
 <222> 217
 <223> Met, Cys, Ile, Leu, Val, Thr or Ser

<220>
 <221> MOD_RES
 <222> 219
 <223> Leu, Val, Met, Thr or Ser

<220>
 <223> each Xaa may also be any amino acid.

<400> 21
 Cys Gly Pro Gly Arg Gly Xaa Gly Xaa Arg Arg His Pro Lys Lys Leu
 1 5 10 15
 Thr Pro Leu Ala Tyr Lys Gln Phe Ile Pro Asn Val Ala Glu Lys Thr
 20 25 30
 Leu Gly Ala Ser Gly Arg Tyr Glu Gly Lys Ile Xaa Arg Asn Ser Glu
 35 40 45 -
 Arg Phe Lys Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys
 50 55 60
 Asp Glu Glu Asn Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys
 65 70 75 80
 Asp Lys Leu Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp Pro Gly
 85 90 95
 Val Xaa Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His His Xaa
 100 105 110
 Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser
 115 120 125
 Asp Arg Asp Xaa Ser Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala Val Glu
 130 135 140
 Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Lys Ala His Ile His Cys
 145 150 155 160
 Ser Val Lys Ala Glu Asn Ser Val Ala Ala Lys Ser Gly Gly Cys Phe
 165 170 175
 Pro Gly Ser Ala Xaa Val Xaa Leu Xaa Xaa Gly Gly Xaa Lys Xaa Val
 180 185 190
 Lys Asp Leu Xaa Pro Gly Asp Xaa Val Leu Ala Ala Asp Xaa Xaa Gly
 195 200 205
 Xaa Leu Xaa Xaa Ser Asp Phe Xaa Xaa Phe Xaa Asp Arg
 210 215 220

<210> 22
 <211> 167

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate
polypeptide sequence

<220>
<221> MOD_RES
<222> 7
<223> Gly, Ala, Val, Leu, Ile, Pro, Phe or Tyr

<220>
<221> MOD_RES
<222> 8
<223> Gly, Ala, Val, Leu or Ile

<220>
<221> MOD_RES
<222> 9
<223> Gly, Ala, Val, Leu, Ile, Lys, His or Arg

<220>
<221> MOD_RES
<222> 12
<223> Lys, Arg or His

<220>
<221> MOD_RES
<222> 13
<223> Phe, Trp, Tyr or an amino acid gap

<220>
<221> MOD_RES
<222> 14
<223> Gly, Ala, Val, Leu, Ile or an amino acid gap

<220>
<221> MOD_RES
<222> 17
<223> Asn, Gln, His, Arg or Lys

<220>
<221> MOD_RES
<222> 19
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 22
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 27
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>

<221> MOD_RES
<222> 29
<223> Ser, Thr, Gln or Asn

<220>
<221> MOD_RES
<222> 30
<223> Met, Cys, Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 31
<223> Gly, Ala, Val, Leu, Ile or Pro

<220>
<221> MOD_RES
<222> 33
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 40
<223> Gly, Ala, Val, Leu, Ile, Pro, Arg, His or Lys

<220>
<221> MOD_RES
<222> 41
<223> Gly, Ala, Val, Leu, Ile, Phe or Tyr

<220>
<221> MOD_RES
<222> 44
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 45
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 46
<223> Thr or Ser

<220>
<221> MOD_RES
<222> 48
<223> Gly, Ala, Val, Leu, Ile, Asn or Gln

<220>
<221> MOD_RES
<222> 53
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 54
<223> Asp or Glu

<220>
<221> MOD_RES
<222> 71
<223> Ser or Thr

<220>
<221> MOD_RES
<222> 79
<223> Glu, Asp, Gln or Asn

<220>
<221> MOD_RES
<222> 83
<223> Glu or Asp

<220>
<221> MOD_RES
<222> 84
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 85
<223> Gly, Ala, Val, Leu or Ile

<220>
<221> MOD_RES
<222> 87
<223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>
<221> MOD_RES
<222> 95
<223> Met, Cys, Gln, Asn, Arg, Lys or His

<220>
<221> MOD_RES
<222> 100
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 107
<223> Trp, Phe, Tyr, Arg, His or Lys

<220>
<221> MOD_RES
<222> 114
<223> Gly, Ala, Val, Leu, Ile, Ser, Thr, Tyr or Phe

<220>
<221> MOD_RES
<222> 115
<223> Gln, Asn, Asp or Glu

<220>
<221> MOD_RES

<222> 116
<223> Asp or Glu

<220>
<221> MOD_RES
<222> 125
<223> Gly, Ala, Val, Leu, or Ile

<220>
<221> MOD_RES
<222> 134
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 135
<223> Asn, Gln, Thr or Ser

<220>
<221> MOD_RES
<222> 139
<223> Gly, Ala, Val, Leu, Ile, Ser, Thr, Met or Cys

<220>
<221> MOD_RES
<222> 141
<223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>
<221> MOD_RES
<222> 157
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 158
<223> Asn, Gln, Gly, Ala, Val, Leu or Ile

<220>
<221> MOD_RES
<222> 160
<223> Gly, Ala, Val, Leu or Ile

<220>
<221> MOD_RES
<222> 162
<223> Gly, Ala, Val, Leu, Ile, Ser, Thr or Cys

<220>
<221> MOD_RES
<222> 166
<223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>
<221> MOD_RES
<222> 167
<223> Asp or Glu

<400> 22

Cys Gly Pro Gly Arg Gly Xaa Xaa Xaa Arg Arg Xaa Xaa Xaa Pro Lys
 1 5 10 15

Xaa Leu Xaa Pro Leu Xaa Tyr Lys Gln Phe Xaa Pro Xaa Xaa Xaa Glu
 20 25 30

Xaa Thr Leu Gly Ala Ser Gly Xaa Xaa Glu Gly Xaa Xaa Xaa Arg Xaa
 35 40 45

Ser Glu Arg Phe Xaa Xaa Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile
 50 55 60

Phe Lys Asp Glu Glu Asn Xaa Gly Ala Asp Arg Leu Met Thr Xaa Arg
 65 70 75 80

Cys Lys Xaa Xaa Xaa Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp
 85 90 95

Pro Gly Val Xaa Leu Arg Val Thr Glu Gly Xaa Asp Glu Asp Gly His
 100 105 110 -

His Xaa Xaa Xaa Ser Leu His Tyr Glu Gly Arg Ala Xaa Asp Ile Thr
 115 120 125

Thr Ser Asp Arg Asp Xaa Xaa Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala
 130 135 140

Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Xaa Xaa His Xaa
 145 150 155 160

His Xaa Ser Val Lys Xaa Xaa
 165

<210> 23

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 23

gcgcgcttcg aagcgaggca gccagcgagg gagagagcga gcgggcgagc cggagcgagg 60

aaatcgatgc gcgc

74

<210> 24

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 24

gcgcgcagat ctgggaaagc gcaagagaga gcgcacacgc acacacccgc cgcgcgact 60
 cgggatccgc gcgc 74

<210> 25
 <211> 996
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: gene
 activation construct

<400> 25
 cgaagcgagg cagccagcga gggagagagc gagcgggcca gccggagcga ggaaatcgaa 60
 ggttcgaatc cttccccac caccatcact ttcaaaagtc cgaaagaatc tgctccctgc 120
 ttgtgtgttg gaggtcgctg agtagtgcgc gagtaaaatt taagctacaa caaggcaagg 180
 cttgaccgac aattgcatga agaatctgct tagggtagg cgttttgcgc tgcttcgcga 240
 tgtaggggcc agatatacgc gttgacattg attattgact agttattaat agtaatcaat 300
 tacgggggtca ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa 360
 tggcccgctt ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt 420
 tcccatagta acgccaatag ggactttcca ttgacgtcaa tgggtggact atttacggta 480
 aactgccac ttggcagtac atcaagtga tcatatgcca agtacgcccc ctattgacgt 540
 caatgacggt aaatggcccg cctggcatta tgcccagtac atgaccttat gggactttcc 600
 tacttggcag tacatctacg tattagtcac cgctattacc atggtgatgc ggttttggca 660
 gtacatcaat gggcgtggat agcggtttga etcacgggga tttccaagtc tccaccccat 720
 tgacgtcaat gggagtttgt tttggcacca aaatcaacgg gactttccaa aatgtcgtaa 780
 caactccgcc ccattgacgc aaatgggagg taggcgtgta cgggtggagg tctatataag 840
 cagagctctc tggctaacta gagaaccac tgcttactgg cttatcgaaa ttaatacgac 900
 tcactatagg gagaccaag cttggtaccg agctcggatc gatctgggaa agcgcaagag 960
 agagcgaca cgcacacacc cgccgcgcgc actcgg 996

<210> 26
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: antisense
 construct

<400> 26
gtcctggcgc cgccgccgcc gtcgcc 26

<210> 27
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: antisense
construct

<400> 27
ttccgatgac cggcctttcg cggatga 26

<210> 28
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: antisense
construct

<400> 28
gtgcacggaa aggtgcaggc cacact 26

<210> 29
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 29
ggctccggta tgtgc 15

<210> 30
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 30
gggtacttc agggc 15

<210> 31
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 31

cattggcagg aggagttgat tgtgg

25

<210> 32

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 32

agcacctttt gaggaggatt tgggg

25